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CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT GCGCCCACAA AATACACTGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC GGGIGCGCAG GCGTATITAG TCGIGCGCCG GCCTCTIGGG GCGTIAGAGA CGCGGGIGIT TTAIGIGGCI GCIACGGGCI AGAIGAAAII CCCGACIIIIG

M etGluGlnAr gGlyGlnAsn AlaProAlaA laSerGlyAl aArgLysArg HisGlyProGly CCGGAAAGG CACGGCCCAG GECETTICO: GTGCCGGGTC GAGAGACTAT AAGAGCGTTC CCTACCGCCA TGGAACAACG GGGACAGAAC GCCCCGGCCG CTTCGGGGGC GAAGCCCCCG 299229999 GGTGCCCGGA CTCTCTATA TTCTCGCANG GGATGGCGGT ACCTTGTTGC CCCTGTCTTG CCACGGGCCT 101

GEOGEGGGGA GECAGGECTG GGCTECGGGT ECECAAGACC CTTGTGCTCG TTGTCGCCGC GGTCCTGCTG TTGGTCTCAG CTGAGTCTGE

ProArgGl uAlaArgGly AlaArgProG lyLeuArgVa lProLysThr LeuValLeuV alValAlaAl aValLeuLeu LeuValSerA laGluSerAla GACTCAGACG CCAGGACGAC AACCAGAGTC GAACACGAGC AACAGCGGCG cosciencer esercesar ecaasecea seserrense 201 GACCCAGGGA CIGGGICCCI

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301 TOTGATCACO CAACAAGACO TAGCTCCCCA GCAGAGAGGG GCCCCACAAC AAAAGAGGTC CAGCCCTCA GAGGGATTGT GTCCACGGG ACACCATATC TGTGGTATAC Leuilethr Ginglnaspi eualaprogi nginargala alaproging inLysargse rserproser gluglyleuc ysproprogi yHisHisile CTCCCTAACA CAGGTGGACC GTCCCCCAGT GINGINCING ANCOAGGGGN CGNCINCCOGGGTGING TITICICCAG AGACTAGTGG

88 SerGluaspc lyargaspcy silesercys lystyrclyc lnasptyrse rthrhistrp asnasplæul euphecyslæ uargcysthr argcysaspser TCAGAAGACG GTAGAGATTG CATCTCCTGC AAATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TITTCTGCTT GCGCTGCACC AGGTGTGATT THACTGGAGG ANARACACGAA CGCGACGTGG TCCACACTAA TITATACCIG ICCIGATAIC GIGAGIGACC GTAGAGGACG CATCTCTAAC AGTOTTOTOC 401

GlyGluVa 1GluLeuSer ProcysThrT hrThrArgAs nThrValCys GlnCysGluG luGlyThrPh eArgGluGlu AspSerProG luMetCysArg TCTACACGGC CACAGIGIGI CAGIGCGAAG AAGGCACCTI CCGGGAAGAA GAIICICCIG CTAAGAGGAC GCCCTTCTT TTCCCTCGAA GTGTCACACA GTCACGCTTC CAGGTGAAGT GGAGCTAAGT CCCTGCACCA CGACCAGAAA GCTGGTCTTT GICCACTICA CCICGAITCA GGGACGIGGI 501

GTAGTAGTAT CATCATCATA yllellelle Lyacyaarg ThrGlyCyap roargGlyMe tvalLysval GlyaspCysT hrproTrpSe raspIleGlu CysvalHisL yaGluSerGl 601 GAAGTGCCGC ACAGGGTGTC CCAGAGGGAT GGTCAAGGTC GGTGATTGTA CACCCTGGAG TGACATCGAA TGTGTCCACA AAGAÁTCAGG CCACTAACAT GIGGGACCTC ACTGTAGCTT ACACAGGTGT ITCTTAGTCC CCAGTTCCAG GGTCTCCCTA TGTCCCACAG CTTCACGGCG

Glyvalthrv alalaalava lvalleulle valalavalp hevalCysly sserLeuLeu TrpLysLysV alLeuProTy rLeuLysGly IleCysSerGly GGAGTCACAG TTGCAGCCGT AGTCTTGATT GTGGCTGTGT TTGTTTGCAA GTCTTTACTG TGGAAGAAG TCCTTCCTTA CCTGAAAGGC ATCTGCTCAG TAGACGAGTC CCTCAGTGTC AACGTCGGCA TCAGAACTAA CACCGACACA AACAAACGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG 701

GlyGlyGl yAspProGlu ArgValAspA rgSerSerGl nArgProGly AlaGluAspA snValLeuAs nGlulleVal SerlleLeuG lnProThrGln GTGGTGGTGG GGACCCTGAG CGTGTGGACA GAAGCTCACA ACGACCTGGG GCTGAGGACA ATGTCCTCAA TGAGATCGTG AGTATCTTGC AGCCCACCCA TCGGGTGGGT TCATAGAACG CITCGAGIGI IGCIGGACCC CGACICCIGI IACAGGAGIT ACTCIAGCAC CACCACCACC CCTGGGACTC GCACACCTGT 807

userprodly GluserGluH isLeuLeuGl uProAlaGlu 901 GGTCCCTGAG CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA CAGGGGGCC CTCAGTCTCG TAGACGACCT GICCITIACC TICAGGICCT CGGICGICIC GGITGICCAC AGTIGIACAA Valproglu GlnGluMetG luValGlnGl uProAlaGlu ProThrGlyV alAsnMetLe

288 Alaciuargs ercinargar gargleuleu Valproalaa anciuciyas pprothrciu Thrleuargo incyspheas pasppheala aspleuvalpro CCTGAAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TGCCACTGAG ACTCTGAGAC AGTGCTTCGA TGACTTTGCA GACTTGGTGC TCACGAAGET ACTGAAACGT CTGAACCACG TGAGACTCTG CGACTTICCA GAGICICCIC CICCGACGAC CAAGGICGIT TACTICCACT AGGGIGACIC 1001







GlyHishrgh spThrLeuTyr CTATGGAAAT gotrogitict agticgitac ctacctticta ggacatticaa aagtgacctg aaccgtaata aaaatatticg acttacacta ttatticctst gataccttta AGCACITITI TAICCIAAIG TAAAIGCIII AIIITAIITAI c**soacctagt aa**ggcaaaca cocatgaaac tctaaaccaa accctacagt aacaaaagtg tcgtgaaaaa ataggattac atttacgaaa taaataaata contecense introcemen áncisgrara ascecracis sactecaste agirgaras iscercarti sicacatsae essircissa asaraetete ggaagggacc aaatggaaaa aagacettty toggettgac etgaggtcag tcatecettyc acggtgttaa cagtgtactg gecatgaccy tetttgagag TRAIGCAGAC ICIGCCMIGI CCIRAGIGIG AITCICITCA GGAAGIGAGA ACCUTCGTC uAlalys6ln CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGTCTG AGADGGAACA GGATTCACAC TAAGAGAAGT CCTTCACTCT TCTCCAACAT TCCCAACCAG GECCACAGGG ACACCTTGTA GAGAGAGACT Threeten ilelystrpy alksnlysth rolyargasp alaservale isthricule uaspalated cluthricus lycluargie CCATCCAACA TCACCCAGIG GAIGGAACAT CCIGIAACIT ITCACIGCAC IIGGCATIAT IIITAIAAGC IGAAIGIGAI AAIAAGGACA CTCTCTCTGA COGGICTCCC phosepse rirpilubro Leumetargi ysleudlyte umetaspasn Gluilelysv alalalysal adlualaala CATGCACAAT BACATAAAGE TGGCTAAAAG TCAGCCACCG TCAACCCGGA GTACCTGTTA CTCTATTTCC ACCGATTTCG ACTOPGTOGC GAGACCCITOG CICIGOGACC LysildGluh apHisleule uSerSerGly LysPheMetT yrLeuGluGl yAsnAlaAsp SerAlaXqqS erDC* CCTACGGAAC GGATGCCTTG INCCOMING GCGIACITIC AGAITIGGIT IGGGAIGICA INGILITICAC ACACCCTGCT occeptor coordached refedences CACCATGCTC ATRANGTOGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC 1301 AAGATTOAGG ACCACTTOTT CAGCTCTGGA AAGPTCATGT ATCTAGAAGG CCITICACIC CIGGGAGCCG CICATGAGGA AGITGGGCCT GAGTACTCCT TATETERCOC ACTIGITATE GRAACTCAG GACCCTCGGC TGGTGAACAA GTOCTACCAC GICIGGAICA TCTAACTCC 388 1101 1401 1501 1601 1201

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AAAAAAAAG GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC

aacccgatgt aacaitctag gtagatgitt fitttititti titttititic cogeegeege tgagatctca getggacgte ittgaaccgg eggtaecgg

TIGGGCTACA TIGIRAGAIC CAICTACAAA AAAAAAAAA

1701

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Scevelsp<u>c</u>tttbntv<u>coceb</u>gtfreedspemcrkcrtgcprgmvkvgdctpwsdiecvh ka<u>sciiigvtvaavvlivavfvcksilm</u>kkvlpylkgicsggggdpervdrssqrpgaed 181

nvinetvsjloptqvpeqemevqepaeptgvrmlspgesehllepaeaeregrrellvpa 241

negdptettrocfddfadlvpfdsweplmrkiglmdneikvakaeaaghrdtlytmlikm vrktgrdasvhtlidaletlgerlakokirdellssgkfmylegnadsals 301

MEPLM IMCVMTLSOVEG VMINA NE NA Apo3/DR3 THERI Apo2 DR4

Fas/Apol

Apo2

DR4

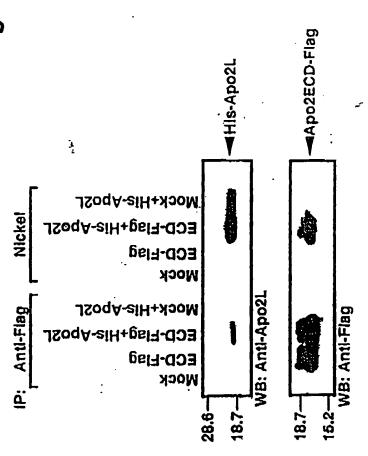
TORIELONGE - CLEBEO

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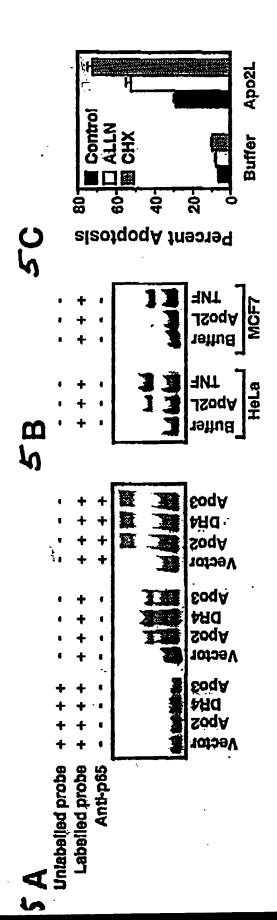


Fig. 5

FIG.6

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kldndey liver lung kldndey

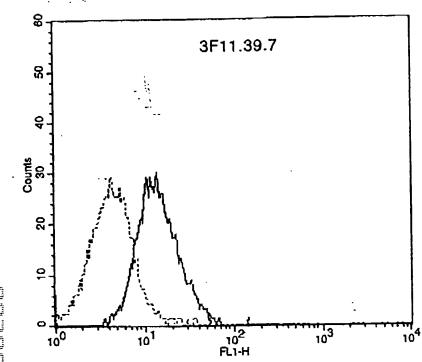


Fig. 7

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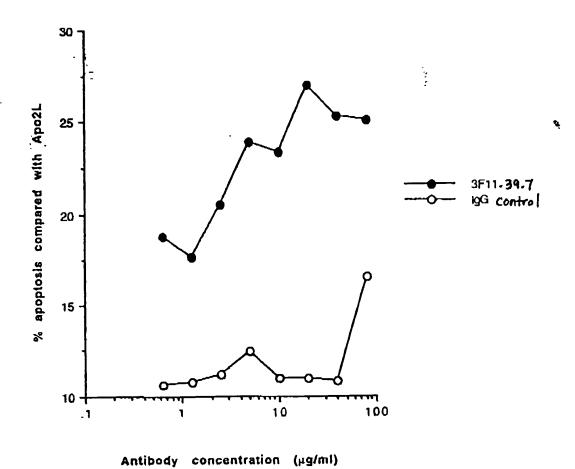


Fig. 8

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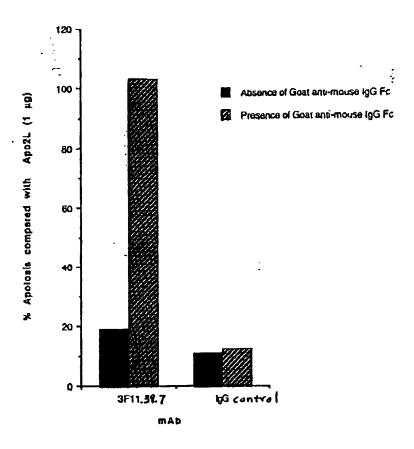


Fig. 9

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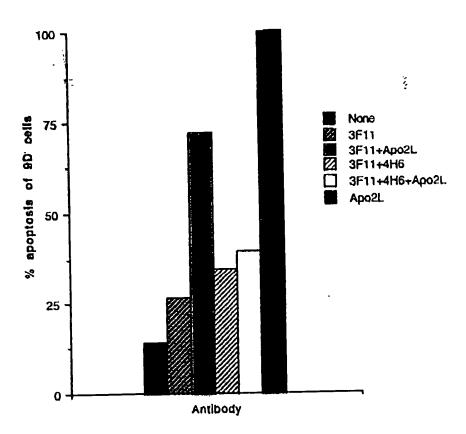


Fig: 10

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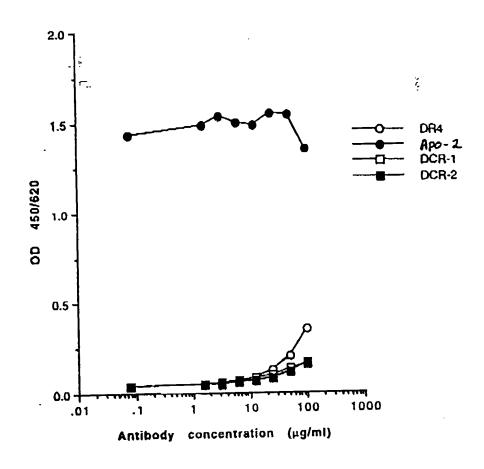


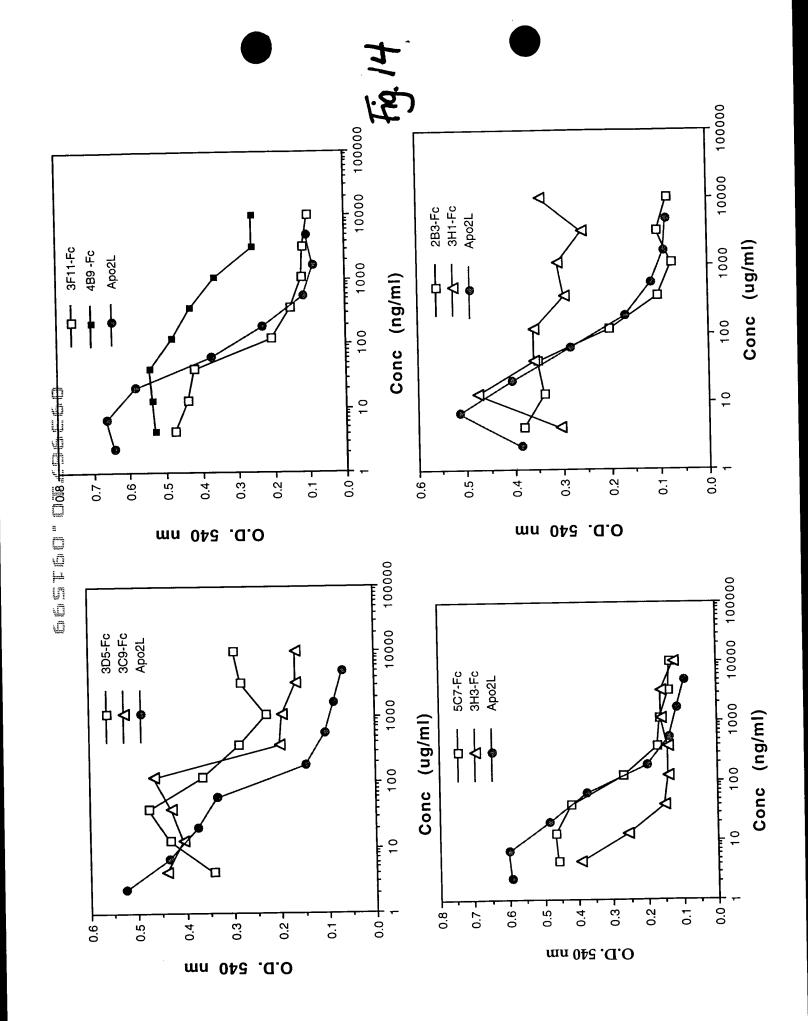
Fig. 11

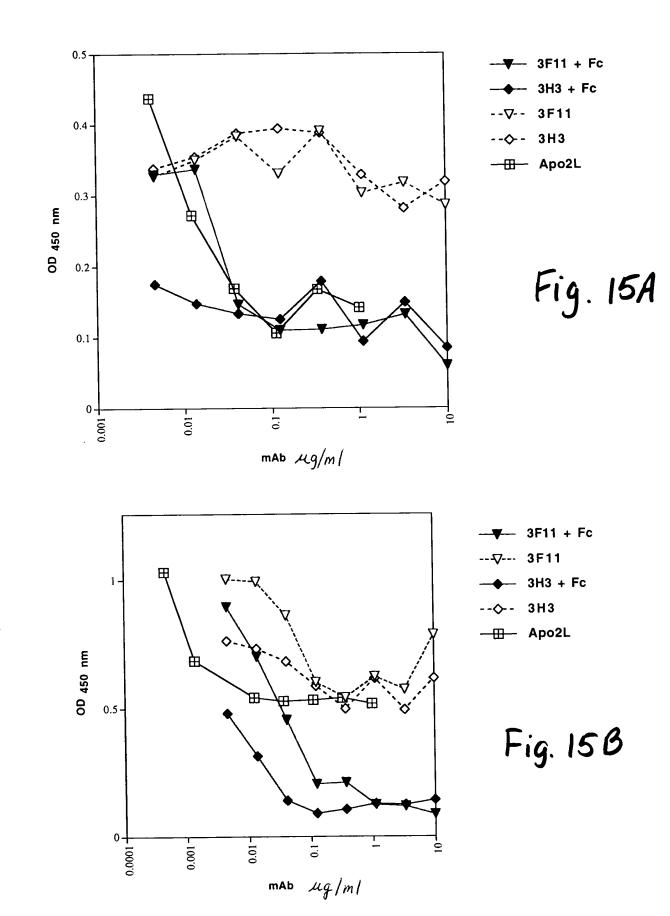
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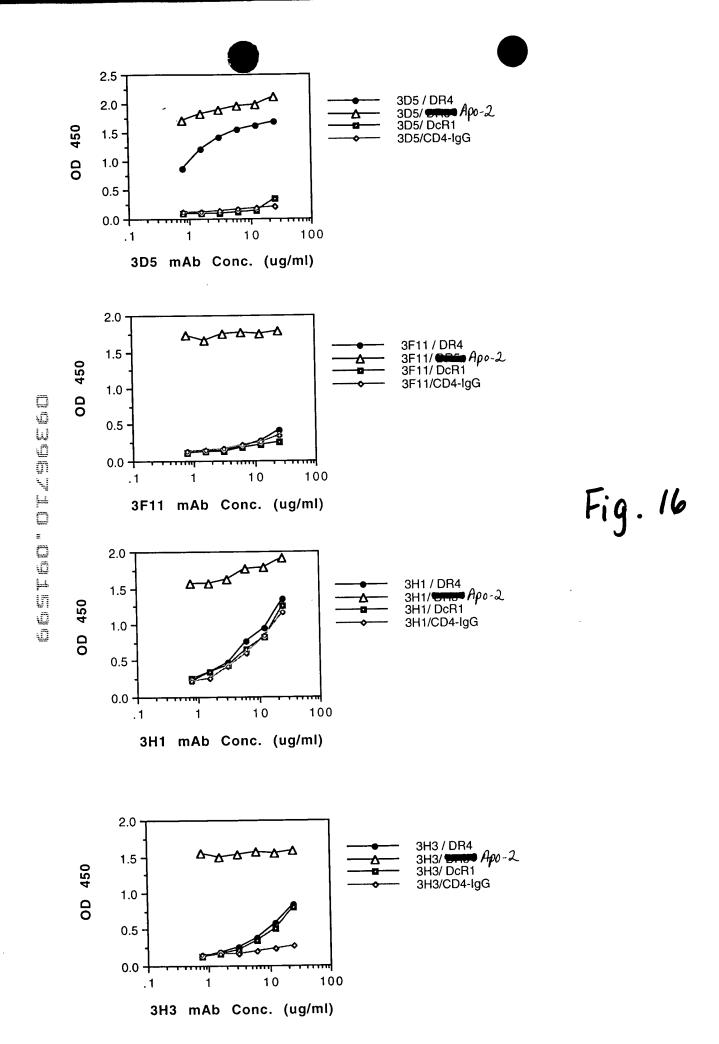
Fig. 12

DR4-IgG to Apo2L Apo-2-IgG to Apo2L	Affinity (pM) 82 1
mAb 3F11 to Apra IgG mAb 3H3 to "	20 3

Fig. 13







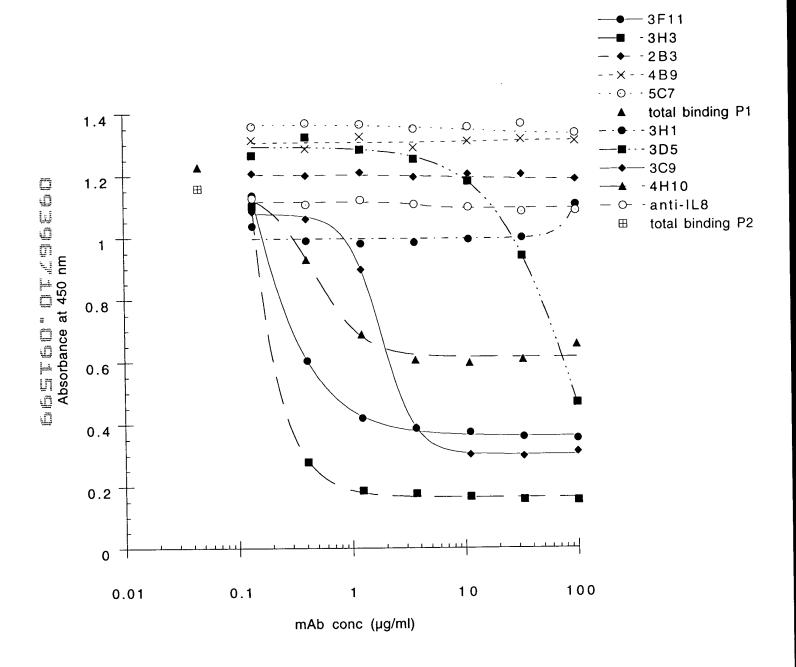


Fig. 17

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Day

Data Collection

ln-house	SSKL
$30-3.5 (3.62-3.50)^a$	30–2.4 (2.49–2.40) ^a
$0.185 (0.398)^a$	0.056 (0.396) ^a
` ,	152,986
•	38,908
99.8 (99.9) ^a	99.8 (99.7) ^a
	30-3.5 (3.62-3.50) ^a 0.185 (0.398) ^a 51,527 12,459

Refinement

Resolution (Å) Number of reflections Final R ^c , R _{free} (F>0) Number of residues Number of solvent molecules Number of non-H atoms Average B factor (Å ²) Rmsd bonds (Å)	30-2.4 38,850 0.222, 0.267 781 286 6577 47.6 0.013
Rmsd bonds (Å)	0.013 1.7
Rmsd angles (°) Rmsd B (bonded atoms) (Å ²)	2.4

^a Numbers in parentheses refer to the highest resolution shell.

Fig. 19

 $[^]b$ R_{sym} = Σ II–<I>I / Σ I. <I> is the average intensity of symmetry related observations of a unique reflection.

 $^{^{}c}$ R = Σ IF_o-F_cl / Σ F_o. R_{free} is calculated as R, but for 10% of the reflections excluded from all refinement.

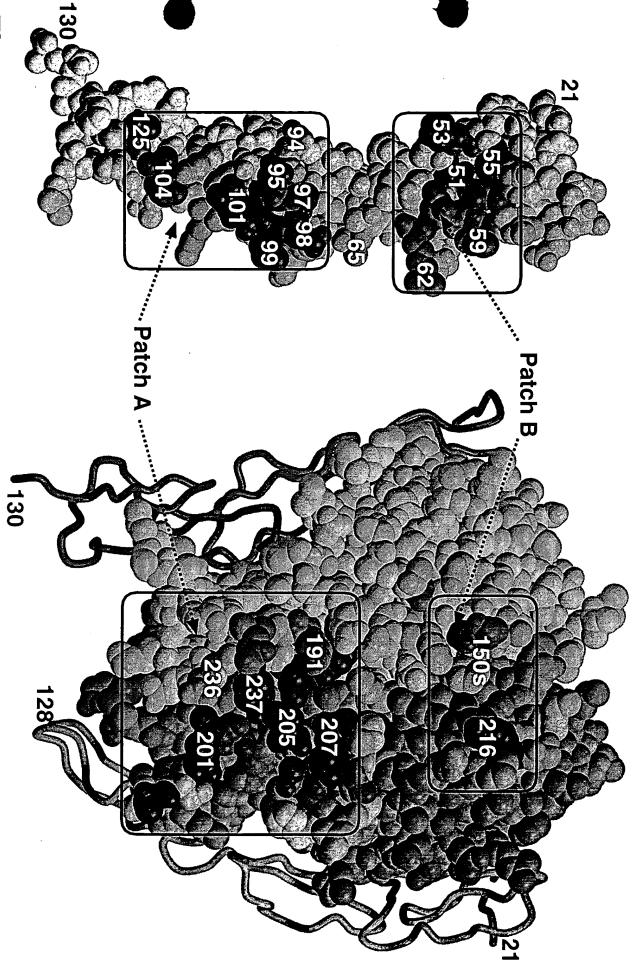


Figure 21

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